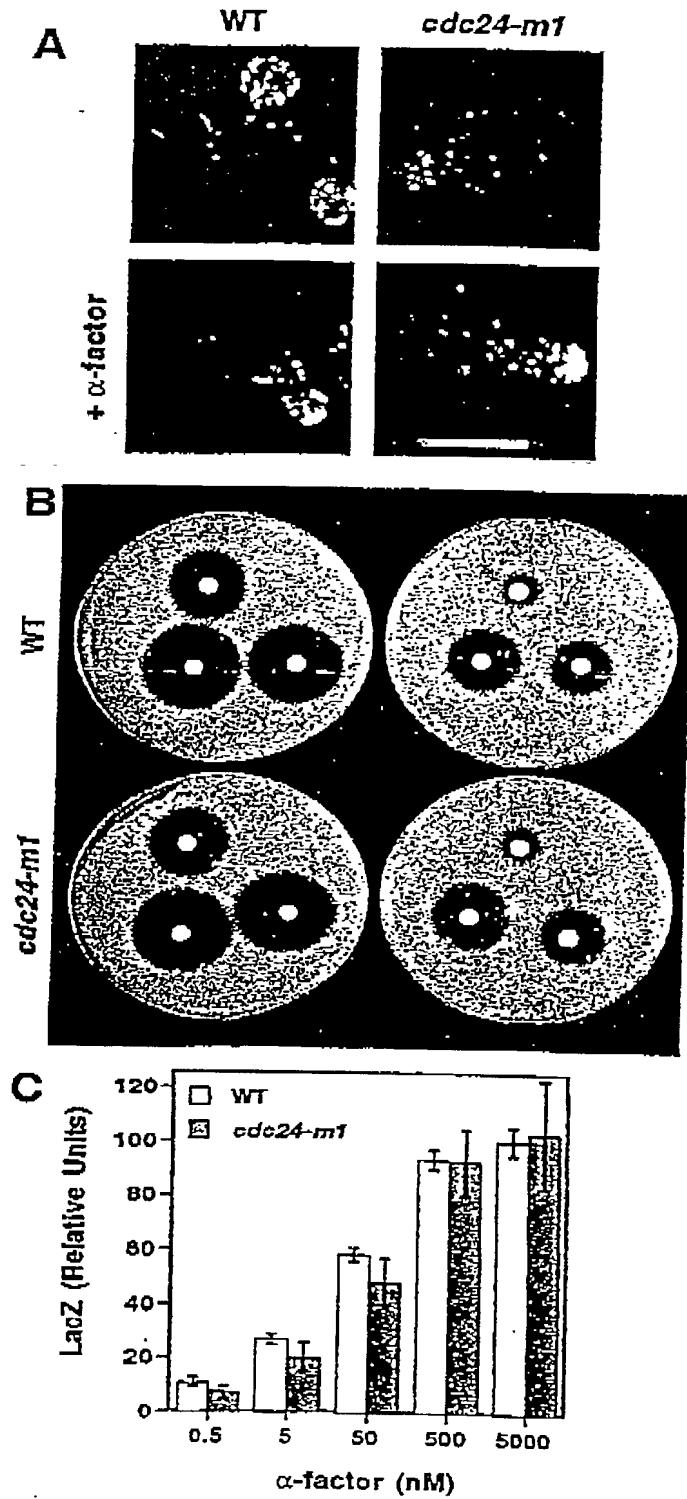
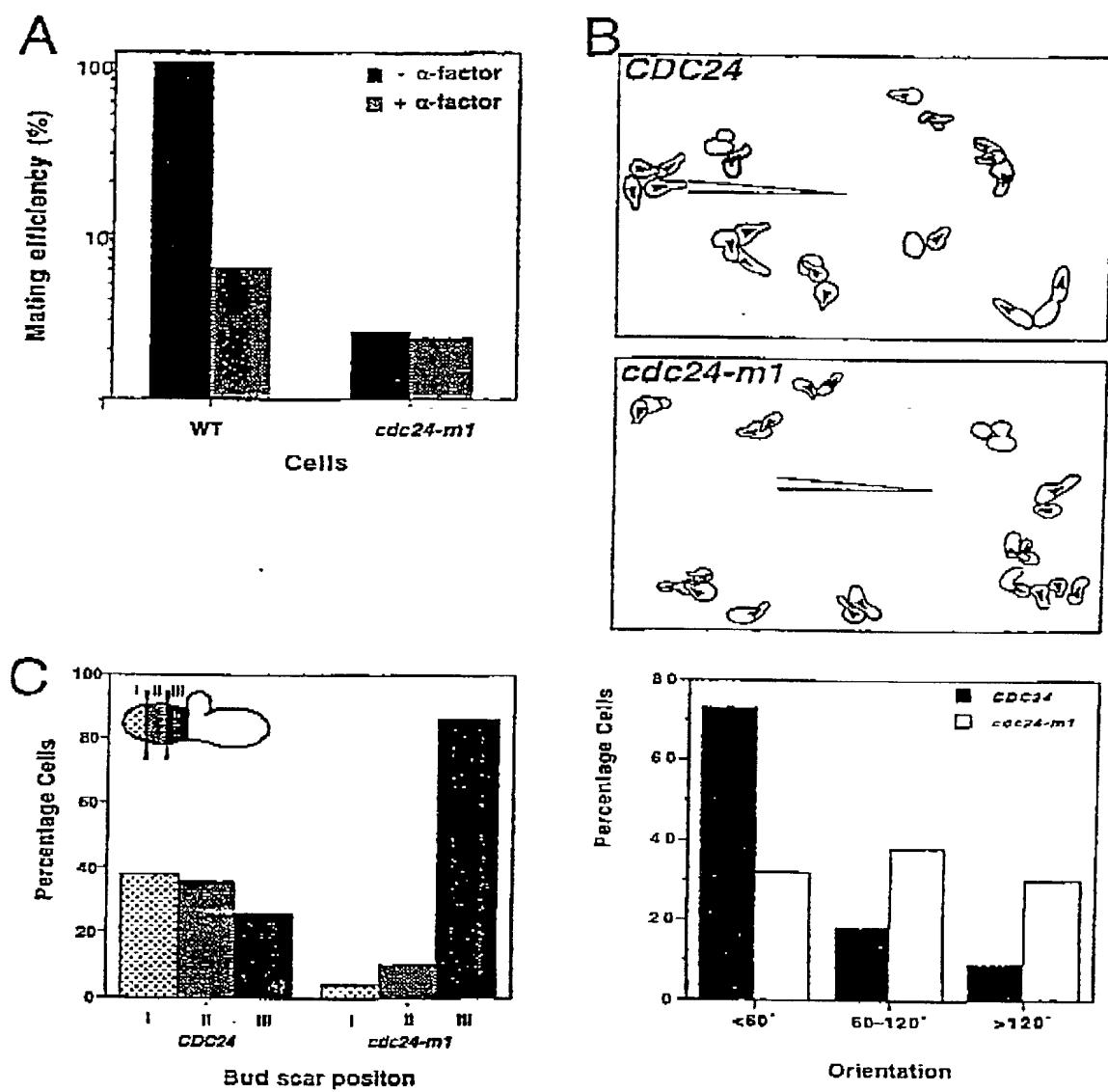


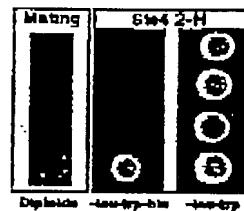
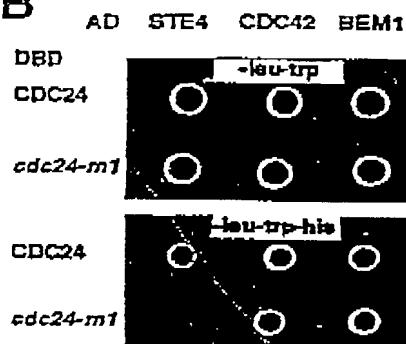
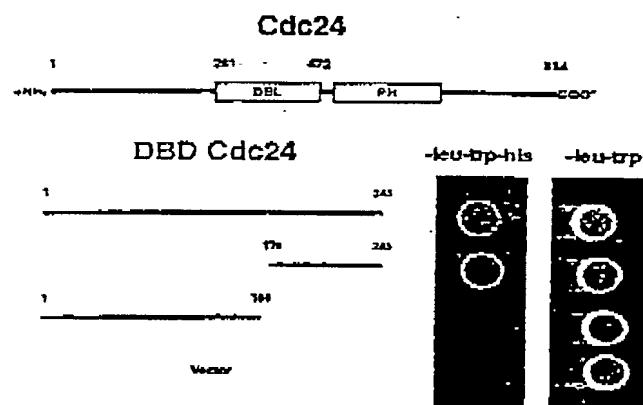
1/24

**FIG. 1**

**FIG. 2**

**A**

Cdc24-m1	QFKLPIVIAFDDLRVKCRKSI
Cdc24-m2	QFKLPIVIAFGDLRKVKRSI
Cdc24-m3	QFKLPIVIAFDDLRVKCRKSI
Ddc24	Se 181 QFKLPIVIAFDDLRVKCRKSI 189  +**   -  *     +  Dd Hu 335 QYEFQVILSPELKVGKRTI 403

**B****C****D**

GST  
GSTCdc24      GST  
GSTCdc24  
Extracts   Eluates

FIG. 3

4/24

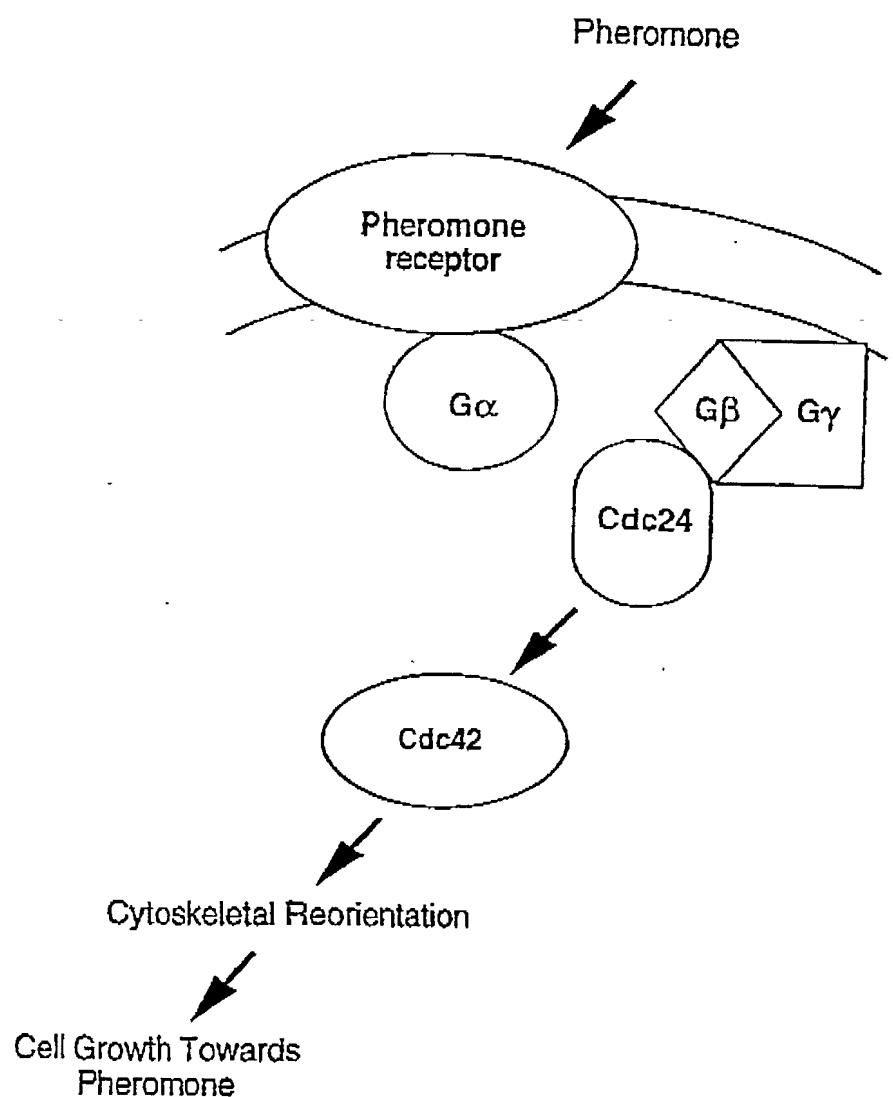


FIG. 4

Figure 5

5	2113/1	2143/11
	ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA M E H P P A A L R T	TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT F S T Q S T S S L N
10	2173/21	2203/31
	TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT S V S T V S S S R I	GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT V S S G P V N I N N
15	2233/41	2263/51
	TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT F N K P S T P K D H	TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA L F Y R C E S L K R
20	2293/61	2323/71
	AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA K L Q K I P G M E P	TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA F L N Q A F N Q A E
25	2353/81	2383/91
	CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG Q L S E Q Q A L A L	GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT A Q E R S N G N G H
30	2413/101	2443/111
	AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC S N G K R H Q S L D	GGT GCC ATG AAT AGA CTT TCA GTT GGT TCT G A M N R L S V G S
35	2473/121	2503/131
	GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA D S S S I Q G S L T	CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT R M A T N A S T S S
40	2533/141	2563/151
	TTA ATC AGT GGT ATG CCA AAC AAC AAC ACT L I S G M P N N N T	TTA TTT ACG TTT ACT GCA GGG GTT TTA CCA L F T F T A G V L P
45	2593/161	2623/171
	GCT AAT ATT AGT GTC GAT CCT GCT ACC CAT A N I S V D P A T H	CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC L W K L P Q Q G A P
50	2653/181	2683/191
	TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT F C V L I N H I L P	GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT D S Q I P V V S S D
55	2713/201	2743/211
	GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT D L R I C K K S V Y	GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG D F L I A V K T Q L
60	2773/221	2803/231
	AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA N F D D E N M F T I	TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT S N V F S D N A Q D
65	2833/241	2863/251
	TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA L I K I I D V I N K	CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC L L A E Y S D A S D
70	2893/261	2923/271
	CTG GGT GGT GGC GAT GAA GAT GTA AAT ATG S G G D E D V N M	GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA D V Q I T D E R S K
75	2953/281	2983/291
	GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA V F R E I I E T E R	AAA TAT GTT CAA GAC TTG GAA CTA ATG TGT K Y V Q D L E L M C
80	3013/301	3043/311
	AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA K Y R Q D L I E A E	AAT TTG TCT TCA GAA CAA ATT CAC TTG TTA N L S S E Q I H L L
85	3073/321	3103/331
	TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT F P N L N E I I D F	CAA AGA CGA TTC CTC AAT GGG TTA CAA TGT Q R R F L N G L E C
90	3133/341	3163/351
	AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA N I N V P I R Y Q R	ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG I G S V F I H A S L
95	3193/361	3223/371
	GGC CCT TTC AAT GCT TAT GAA CCT TGG ACT G P N A Y E D W T	ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC I G Q L T A I D L I
100	3253/381	3283/391
	AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG N K E A A N L K K S	TCA AGT CTA CTT GAT CCT GGG TTT CAA CTT S S L L D P G F E L
105	3313/401	3343/411
	CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA Q S Y I L K P I Q R	TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG L C K Y P L L L K E
110	3373/421	3403/431
	TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA L I K T S P E Y S K	CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA Q D P H G S S S S T
115	3433/441	3463/451
	TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT S F N E L L V A K T	GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT A M K E L A N Q V N

6/24

3493/461  
 GAG GCG CAA AGA CGA GCA GAA AAT ATC GAA CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT  
 E A Q R R A E N I E H L E K L K E R V G  
 3553/481  
 5 AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG  
 N W R G F N L D A Q G E L L F H G Q V G  
 3613/501  
 GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT  
 V K D A E N E K E Y V A Y L F E K I V F  
 10 3673/521  
 TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT  
 F F T E I D D T K K S D K Q E K K S K F  
 3733/541  
 TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA  
 15 S T R K R S T S S N L S S S T T N L L E  
 3793/561  
 TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT  
 S I N N S R K D N T L P L E L K G R V Y  
 3853/581  
 20 ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA  
 I S E I Y N I S A P N T P G S T L I I S  
 3913/601  
 TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA  
 W S G R K E S G S F T L R X R S E E A R  
 25 3973/621  
 AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT  
 N Q W E K C L R D L K T N E M N K Q I H  
 4033/641  
 AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC  
 30 K K L R D S D S S F N T D D S A I Y D Y  
 4093/661  
 ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG  
 T G I S T S P V N Q S T Q Q Y Y D H R  
 4153/681  
 35 GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT  
 G S H S S R H H S S S T L S M M K N N  
 4213/701  
 AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC  
 R V K S G D L S R I S S T S T T L D S F  
 40  
 4273/721  
 AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC  
 S N N L N G S P N T T N P S L M S S D A  
 4333/741  
 45 ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG  
 T K T I P T F D V A I K L L Y K S T E L  
 4393/761  
 4423/771  
 TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC  
 S E P L I V N A Q I E Y N D L L Q K I I  
 4453/781  
 50 TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT  
 S Q I I T S N L V A D D V N I S R L R Y  
 4513/801  
 4543/811  
 AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG AAT TCA GAT GAT GAT TGG GGG TTA GTG CTT  
 K D D E G D F V N L N S D D D W G L V L  
 55 4573/821  
 4603/831  
 GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA  
 D M L T S E D F Y Q T S S N E K R S V T  
 4633/841  
 GTG TGG GTT TCT TGA  
 60 V W V S \*

7/24

Figure 6

5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1	MAIQ---TR-FA M R F+	8
C.a. Cdc24p: 1	MEHPPAALRTFSTQ	14
10 S.c. Cdc24p: 9	SGTSLSDLKPKPSATSISYPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPOLKPFQLQ	66
	S+SL+ + S+ N+ NKP T +D LF+ C +++++L+ +P ++PFL	
C.a. Cdc24p: 15	STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLYRCESSLKRKLQKIPGMEPPLNQ	74
15 S.c. Cdc24p: 67	AYQSSEVLSERQSLLLSQKQHQELLKSNGANRDSSDLAP---TLRSSSISTATSLMSMEG	123
	A+ +E LSE+Q+L L+Q++ SNG S D A + + S S S SL M	
C.a. Cdc24p: 75	AFNQAELSEQQALALAQERSNGNGHSNGKRHQSLDAMNRSLVGSDSSSIQGSLTRMAT	134
20 S.c. Cdc24p: 124	ISYTNNSNPSPATPNMEDTLLTFMSMGILPITMDCDFVTQLSQLFQQGAPLCLIFNSVKPQFK	183
	+ T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +	
C.a. Cdc24p: 135	NASTSSLISCGMPN-NNTLFTFTAGVLPANISVDPATHLWKLFPQQGAPFCVLINHILPDSQ	193
S.c. Cdc24p: 184	LPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQLVKVLEVETLMN	243
	+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K++V+ L+	
25 C.a. Cdc24p: 194	IPVVSSDDLRICKKSVDLIAVKTQLNFDDENMFTISNVFSDNAQDLIKIIDVINKLLA	253
S.c. Cdc24p: 244	SSPTIFPSKSQTQQIMNAENQHRQPQQSKKHNEYVKIIKEFVATERKYVHDLEILDKY	303
	S + + + + + E K+ +E + TERKYV DLE++ KY	
C.a. Cdc24p: 254	EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIITERKYVQDLELMCKY	302
30 S.c. Cdc24p: 304	RQQLLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQRIGALFMH-SKHF	362
	RQ L+++ +SE++++LFPNL + IDFQRRFL LE N V QRIQ++F+H S	
C.a. Cdc24p: 303	RQDLIEAENLSSEQIHLFPNLNEIIDFQRRFLNGLECNIINVPIRYQRIGSVFIHASLG	362
35 S.c. Cdc24p: 363	FKLYEPWSIGQNAATEFLSSTLHOMRVDESQRFIINNKLELQSFYKPVQRLCRYPLLVK	422
	F YEPW+IGQ AI+ ++ ++ S +++ ELOQ++ KP+QRLC+YPLL+K	
C.a. Cdc24p: 363	FNAYEPWTIGQLTAIDLINKEAANLKKSS--LLDPGFELQSYILKPIQRACKYPLLK	419
40 S.c. Cdc24p: 423	ELLAE-----SSDDNNNTKELEALDISKNIARSINENQRRTENHQVVKKLYGRV	471
	EL+ SS + EL A K+A +NE QRR EN + ++KL RV	
C.a. Cdc24p: 420	ELIKTSPEYSKQDPHGSSSSTSFnELLVAKTAMKELANQVNEAQRRAEINIELEKLKERV	479
S.c. Cdc24p: 472	VNWKGYRISKPGELLYFDKVFISSNSEPREFEVYLFEKILLLFSEVVTKKSASSLI	531
	NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K+	
45 C.a. Cdc24p: 480	GNWRGFNLDAQGELLFHGQVGV---KDAENEKEYVAYLFEKIVFFFTEIDDTKKSDKQE	535
S.c. Cdc24p: 532	LKKKSSTSASISASNITDNNGSPHHSYHKKRHNSSSSNNIHLSSSSAAIIHSSTNSSDN	591
	K K ST ++SN+ SSS ++ S NS +	
C.a. Cdc24p: 536	KKSFKSTRKRSTSSNL-----SSSTNLLESINNSRKD	568
50 S.c. Cdc24p: 592	NSNNSSSSLFKLSANEPKLDLGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK	649
	N+ L+L+GR+ I + I N +L I+W KE G+F+L+	
C.a. Cdc24p: 569	NT-----LPLELKGRVYIISIYNISAPNTPGSTLIISWSGRKESGSFTLR	613
55 S.c. Cdc24p: 650	FKNEETRDNWSSCLQQLIHDLKNEQFKARHHSSTSTTSS-----TAKSSSMSPTTT	701
	+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T	
C.a. Cdc24p: 614	YRSEEARNQWEKCLDLKTNEMNKQIHKKLRSDFSSFTDDSAIYDYGISTSPVNQSTQ	673
S.c. Cdc24p: 702	MNTPNHNSRQT--HDSMASFSSSHMKRVS---DVLPKRRTTSSFESEIKS-----	748
	+H S + H S ++ S RV + TT SF + +	
C.a. Cdc24p: 674	QQYYDHRGSHSSRHHSSSSTLSMMKNNRVRKGDLRSISSTTLDLFSNNLNGSPNTTNP	733
S.c. Cdc24p: 749	--ISENPKNNSIPESSILFRISYNNNSNNTSSEIFTLLVEKWNFDDLIMAINSKI--SN	804
	+S + +IP + ++ Y +T SE L+V + +DL+ I S+I SN	
65 C.a. Cdc24p: 734	SLMSSDATKTIPTFDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKIIQIITSN	787
S.c. Cdc24p: 805	THNNNISPITKIKYQDEDGDFVVLGSDEDWNVAKEMLAENNEKFLNIRLY	854
	++++ I++++Y+D++GDFV L SD+DW + +ML + F +	
C.a. Cdc24p: 788	LVADDVN-ISRLRYKDDEGDFVNLSDDDWGLVLDMLTSED--FYQTSSNEKRSVTWWV	844

Figure 7a

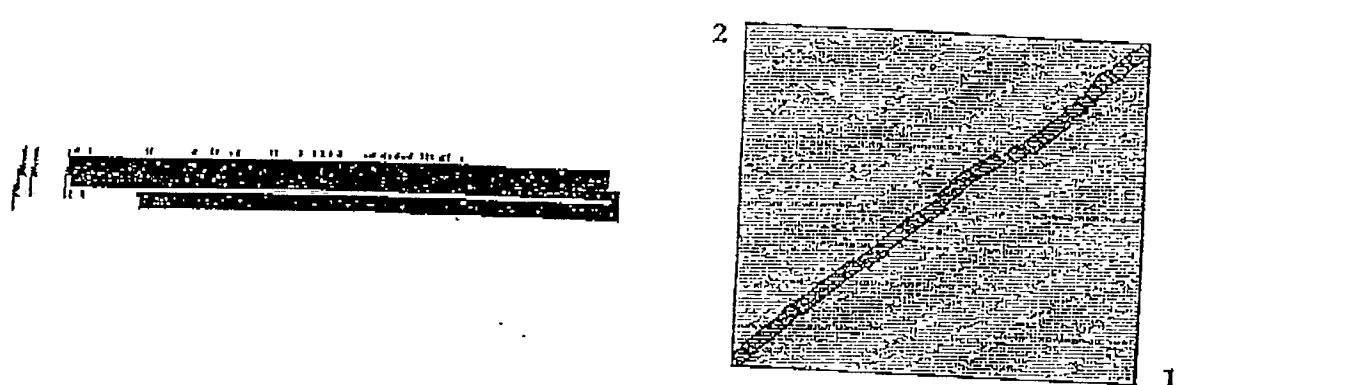
8/24

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

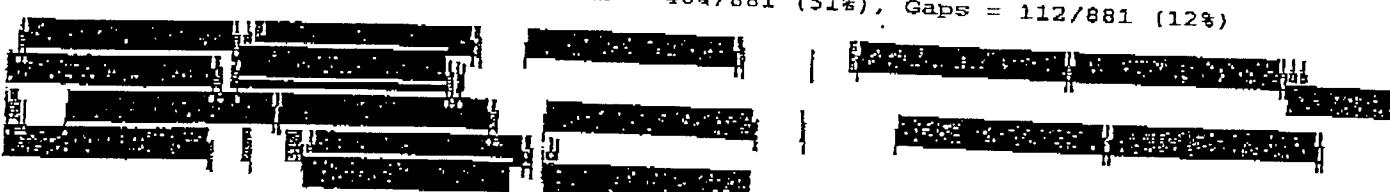
Matrix **0 BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter  Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1 .. 854)

Sequence 2 lcl|C.a. Cdc24p Length 844 (1 .. 844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database  
Score = 446 bits (1136), Expect = e-124  
Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)



Query: 9 SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLPHICANIRKRLEVL PQLKPFQLQL 66  
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL  
Sbjct: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEEFPLNQ 74

Query: 67 AYQSSEVLSEROSILLLSQKQHQELLKSNGANRDSSDLAP---TLRSSSISTATSLMSMEG 123  
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M  
Sbjct: 75 AFNQAEQLSEQOALALAQERSNGNGHSNGKRHQSLDGAMNRLSVGSDSSSIQGSLTRMAT 134

Query: 124 ISYTNSNPSATPNMEDTLTFSMGILPITMDCDPVTQLSQLFQQGAPLCILFNSVKPQFK 183  
+ T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +  
Sbjct: 135 NASTSSLISGMPN-NNTLFTFTAGVLPANISVDPATHLWKLFFQQGAPFCVLINHILPDSQ 193

Query: 184 LPVIASDDLKVCKKSITYDFILGCKKHFAFNDEELFTISDVFANSTSOLVKLEVETLMN 243  
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+  
Sbjct: 194 IPVVSSDDLICKSVYDFLIAVKTQLNFDDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

Query: 244 SSPTIFPSKSKTQQIMNAENQHRHQPQQSSKKHNEYVKIIKEFVATERKYVHDLEILDKY 303  
S + + + + + E K+ + E + TERKYV DLE++ KY  
Sbjct: 254 EYSDASDGGGDEDV-----NMDVQITDERSKVFREIIETERKYVQDLELMCKY 302

Query: 304 RQQLLDNSNLITSEELYMLFPNLGDAIDFORRFLISLEFINALVEPSKQRIGALFMH-SKHF 362  
RQ L++- ++SE++++LFPNL + IDFQRRFL LE N V QRIG++F+H S  
Sbjct: 303 RQDLIEAENLSSEQIHLFPNLNEIIDFQRRFLNGLECNINVPIRYQRIGSVFIASLGP 362

Query: 363 FKLYEPWSIGQNAAI2FLSSTLHKMRVDESQRFTINNKLELQSFYKPVORLCRYPLLVK 422  
F YEPW+IGQ AI+ ++ + S +++ ELQSt+ KP+QRLC+YPLL+K  
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS--LLDPGFELQSYILKPIQRLCKYPLLK 419

F Figure 7a cont.

9/24

Query: 423 ELLAE-----SSDDNNNTKELEAALDISKNIARSTINENQRRTENHQVVKKLYGRV 471  
 EL+ SS + EL A K +A +NE QRR EN + ++KL RV  
 Sbjct: 420 ELIKTSPEYSKQDPHGSSSSTSZNELLVAKTAMKELANQVNEAQRRRAENTIEHLEKLKERV 479

Query: 472 VNWKGYRISKFGELLYFDKVFI STMNSSEPEREFEVYLFEKIIILFSEVVTKKSASSLI 531  
 NW+G+ + CELL+ +V+ +E E+E+ YLFEKI+ F+E+ K+  
 Sbjct: 480 GNWRGFNLDAQGELLFHGQVGV---KDAENEKEYVAYLFEKIVFFTEIDDTKKSDKQE 535

Query: 532 LKKKSSTSASISASNITDNNGSPHSYHKRHNSSSSNNIHLSSSSAAATIHSSTNSSDN 591  
 K K ST ++SN+ SSS + + S NS +  
 Sbjct: 536 KKSKF5TRKRSTSSNL-----SSSTNLLESINNSRKD 568

Query: 592 NSNNSSSSSLPKLSANEPKLDLRGRIMIMMNQIIPQN--NRSLNITWESIKEQGNFLLK 649  
 N+ L+L+GR+ I + I N +L I+W KE G+F L+  
 Sbjct: 569 NT-----LPLELKGRVYISEIYNISAPNTPGSTLTISWSGRKESGSPTLR 613

Query: 650 FKNEETRDNWSSCLQQQLIHDLKNEQFKARHHSSTTTSS-----TAKSSSMMSPTTT 701  
 +-+2E R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T  
 Sbjct: 614 YRSEEARQWEKCLRDLKTNEMNQIHKKLRLDSDSSFTTDSAIYDYTGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS---DVLPKRRTTSSSFSESEIKS----- 748  
 +H S + H S ++ S RV + TT SF + +  
 Sbjct: 674 QQYYDHRGSHSSRHSSSTLSMMKQNRVKSGDLSRISSTTLDSPSNNLNGSPNTTNP 733

Query: 749 --ISENFKN SIPESSILFRISYNNNSNNTSSSEIFTLLVEKVWNFDLIMAINSKI--SN 804  
 +S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN  
 Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKIIISQIITSN 787

Query: 805 THNNNTSPITKIKYQDEDGDFVVLGSDEDWNVAKEMLAENN 845  
 +++ I+ + +Y+D++GDFV L SD+DW + +ML +  
 Sbjct: 788 LVADDVN-ISRLRYKDDEGDFVNLSDDDWGLVLDMLTSED 827

CPU time: 0.26 user secs. 0.02 sys. secs 0.28 total secs.

Gapped  
 Lambda K H  
 0.270 0.0470 0.230

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 12253  
 Number of Sequences: 0  
 Number of extensions: 709  
 Number of successful extensions: 15  
 Number of sequences better than 10.0: 1  
 Number of HSP's better than 10.0 without gapping: 1  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 1  
 length of query: 844  
 length of database: 90,077,593  
 effective HSP length: 63  
 effective length of query: 781  
 effective length of database: 83353792  
 effective search space: 65099311552  
 effective search space used: 65099311552  
 T: 9  
 A: 40  
 X1: 16 ( 7.2 bits)  
 X2: 128 (49.9 bits)  
 X3: 128 (49.9 bits)  
 S1: 42 (21.9 bits)  
 S2: 73 (32.8 bits)

Figure 7b

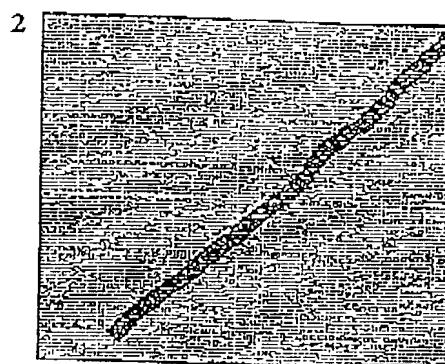
10/24

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix  BLOSUM62 gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 Icl|S.c. Cdc24p Length 854 (1 .. 854)

Sequence 2 Icl|S.p. Cdc24p Length 834 (1 .. 834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61  
Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)



Query: 156 DPVTQLSQLFQQGAPLCILFNSVKPQFKLPVIASDDLK---VCKKSITYDFILGCKKHFAF 212  
DPVT++ + G PLC LEN + + KL V + S L+ VCK S+Y F+L CK  
Sbjct: 67 DPVTEIWLFTRLGYPLCALFNCLPVKQKLEVNSSVSLENTNVCKASLYRFMLMCKNELGL 126

Query: 213 NDEELFTISDVFANSTSSQLVKLEVETLMNNSPTIFPSKSKTQQIMNAENQERHQPOQS 272  
D LF+IS+++ ST+ LV+ L+ +E L+ +KS + + ++ S  
Sbjct: 127 TDAALFSISEIYKPSTAPLVRALQTIELLLKKYEVSNTTKSSTPSPSTDDNVPTGTLNS 186

Query: 273 SKKHNEYVKITKEFVATERKYVADLEILDKYRQQQLDSNLITSEELYMLFPNLGDAIDFQ 332  
++ E TE KY+ DLE L Y L + + + + +F NL + +DFQ  
Sbjct: 187 LIASGR--RVTAELYETELKYIQDLEYLSNYMVLQQKQILSQDTILSIFTNLNEILDFQ 244

Query: 333 RRFLISLEINALVEPSKQRIGALFMHSKHFFKLYEPWSIG-QNAATFLLSSTLHKMRVDE 391  
RRFL+ LE+N + +QR+GALF+ + F +Y+ + NA + + + +V  
Sbjct: 245 RRFLVGLEMNLSLPVEEQLCIALLEGFSVYQVFCTNFPNAQQLIIDNQNQQLKVN 304

Query: 392 SQRFIINNKLELQSFYKPVQLCRYPLLKELL-AE55DDNNNTKELEAALDISKNTARS 450  
++ EL + L KP+QR+C+YPLL+ +LL S +EL+ + +A  
Sbjct: 305 ---LLEPSYELPALLIKPIORICKYPLLNLQNLKGTPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRRTENHQVVKLYGRVVNWKGYRISKFGELLYFDKVPISTTNSSEPEREFEVYL 510  
+NE +R EN + +L RV++WKGY + FG+LL +D V + + ERE+ VYL  
Sbjct: 361 VNETRRIHENRNAIIIELEQRVIDWKGYSLQYFGQLLVWDVVNV---CKADIERYHVYL 416

Query: 511 FEKIIILFSEVVT-KKSASSLILKKKSSTSAS-----ISASNITDN----- 550  
FEKI++ E+ T K+ A S+ + KK+ S I SNIT  
Sbjct: 417 FEKILLCCKEMSTLKQARSISMNKKTKLDSLQLKGRILTSNITTVPNHHMGSYAIQI 476

| Figure 7b cont..

11/24

Query: 551 --NGSPHHSYHKRHNSSSNNIHL-----SSAAAIHSSTNSDNNNNSSS 599  
G P H + S+ + +S + I S+ ++ N N SSS  
Sbjct: 477 FWRGDPQHESFILKLRNEESHKLWMSVLNRLLWKNEHGSFKDIRSAASTPANPVYNRSSS 536

Query: 600 SLFKLSANEPKLD-LRGRIMIMNLN---QIIPQNNRSLNITWESIKEQGNFLKFKNEET 655  
K N D LR + N+N I +++S T + K+ K+ T  
Sbjct: 537 QTSK-GYNSSDYDLRTHSLDENVNSPTSISSPSSKSSPFTKTTSKDT-----KSATT 588

Query: 656 RDNWSSCLQQLIHDLKNEQFKARHHSSTST-----TSSTAKSSSMSPTTMNT--PNHH 708  
D S +L + R +TST +SSTA S+S + +N+ +++  
Sbjct: 589 TDERPSDFIRLNSEESVGTSLSRSTSQTTSIVSNDSSSTASIPSQISRKISQVNSSLINDYN 648

Query: 709 NSRQTH-----DSMASF---SSSHMKRVSD-----VLPKRRRTTSSSFSE 745  
+RQ+H S++ F SSS +++ D + P++ + S+ +S+  
Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708

Query: 746 IKSIENFKNSIPESSILFRISYNNNSNNTSSSEI---FTLLVEKVWNFDLIMAINSK 801  
+ S+ SS + S N +N + L+V FD+L+ + K  
Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLHEVSLVLUVARDITFDELLAKVERK 768

Query: 802 IS--NTHNNNISPITKIKYQDEDGDFVVLGSDEDWNVAKE 839  
I + ++KY DEDGDF+ + SDED +A E  
Sbjct: 769 IKLCGILKQAVPPRVRKLYVDEDGDFITITSDEDVILMAFE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.  
Gapped  
Lambda K H  
0.270 0.0470 0.230

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 10384  
Number of Sequences: 0  
Number of extensions: 671  
Number of successful extensions: 13  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 2  
Length of query: 834  
length of database: 90,077,593  
effective HSP length: 61  
effective length of query: 773  
effective length of database: 83489227  
effective search space: 64537172471  
effective search space used: 64537172471  
T: 9  
A: 40  
X1: 16 ( 7.3 bits)  
X2: 128 (49.9 bits)  
X3: 128 (49.9 bits)  
S1: 41 (21.7 bits)  
S2: 73 (32.8 bits)

12/24

Figure 8

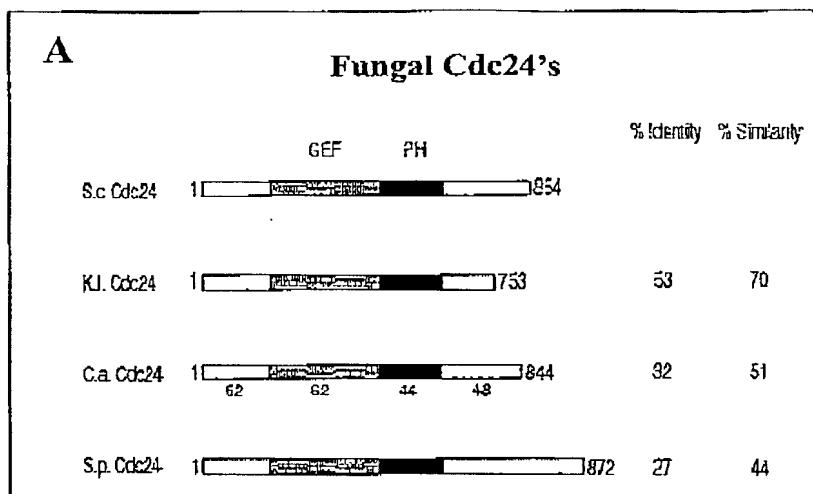
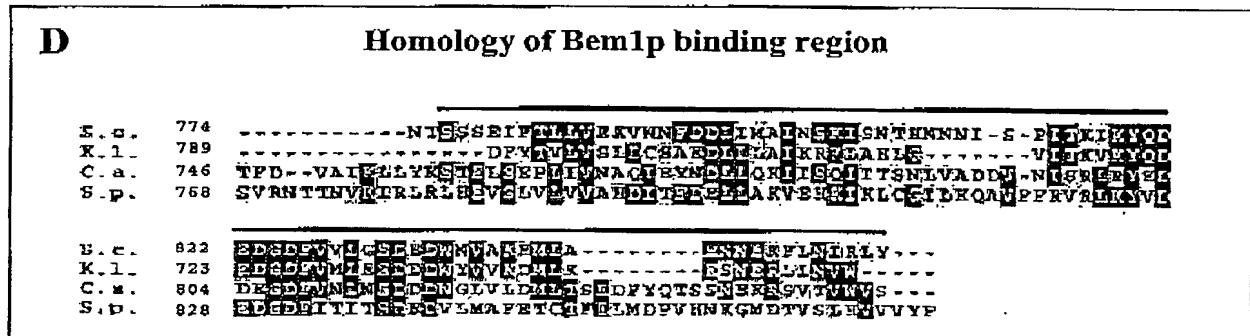
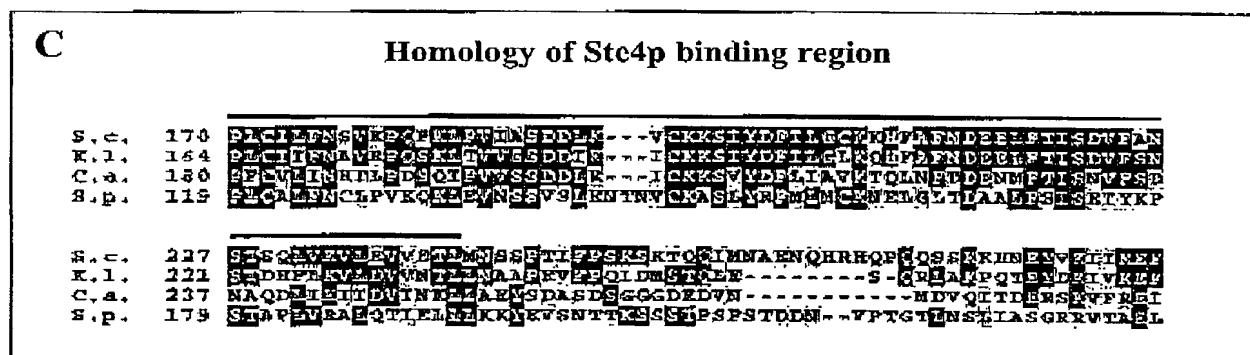
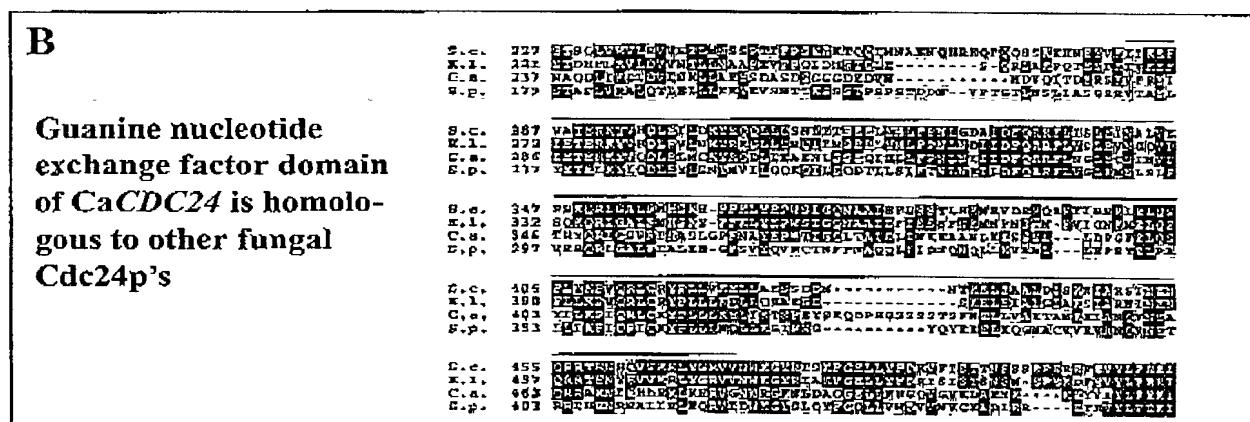
5 Sc KLPVIASDDLKVCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

Ca QIPVVSSDDLICKKSVYDFLI (SEQ ID No 26)

10 Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

**figure 9**

14/24

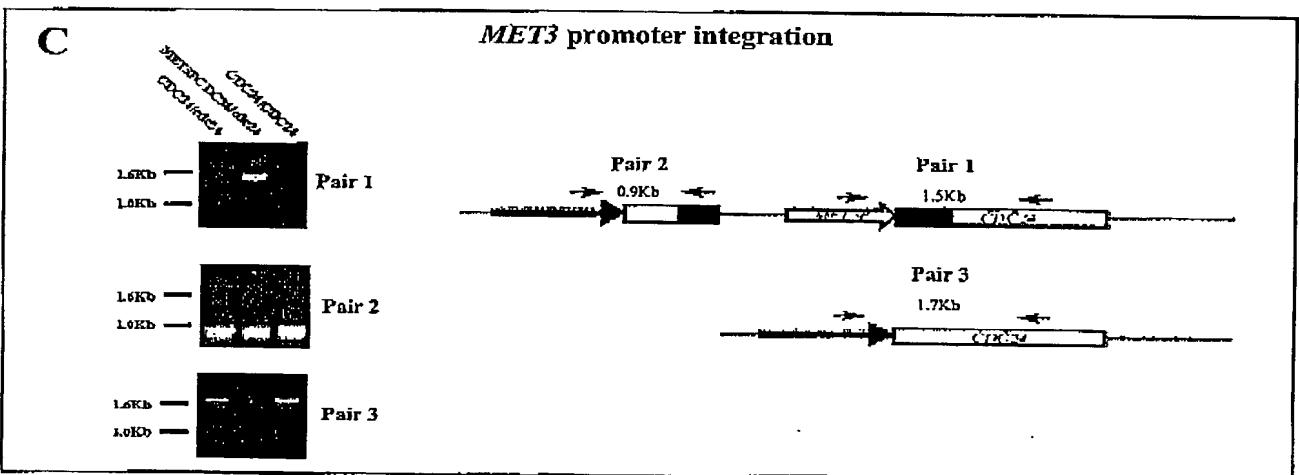
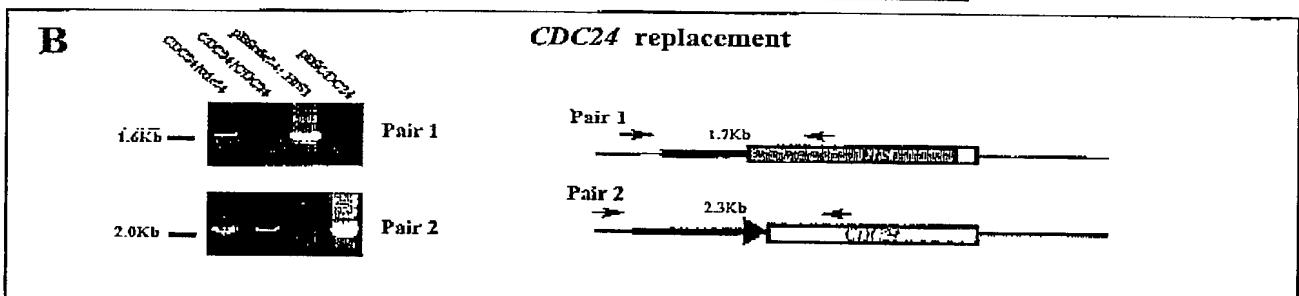
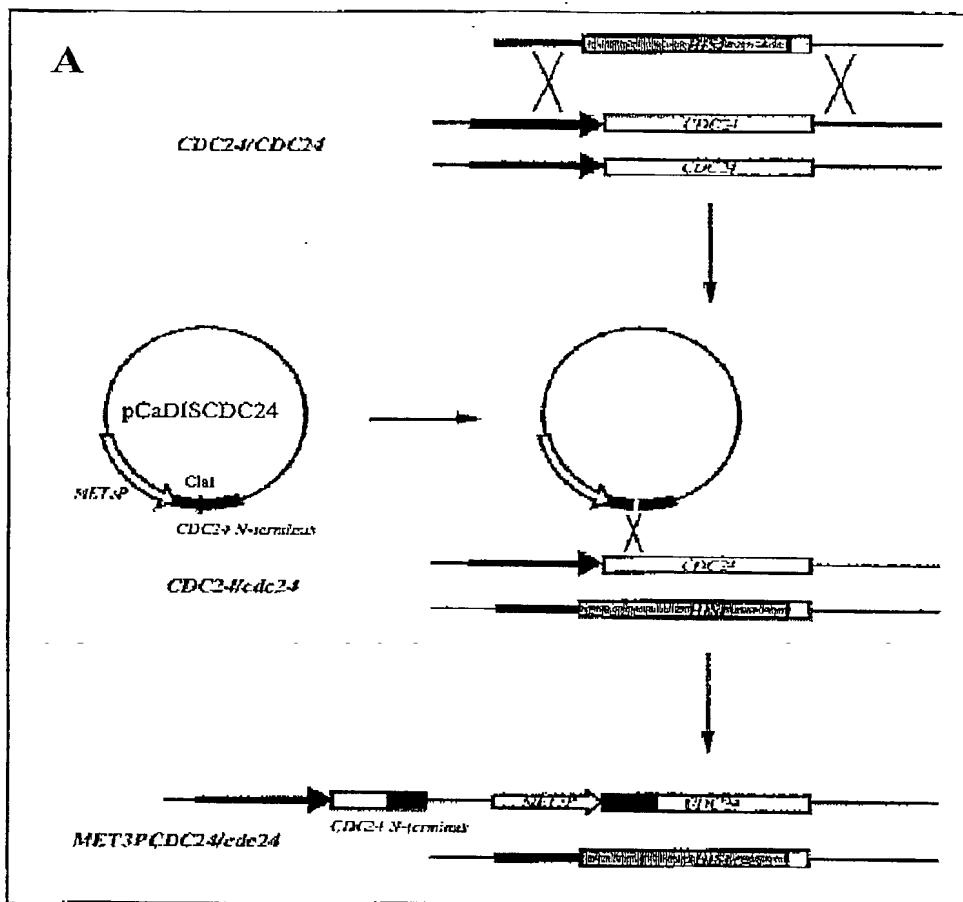
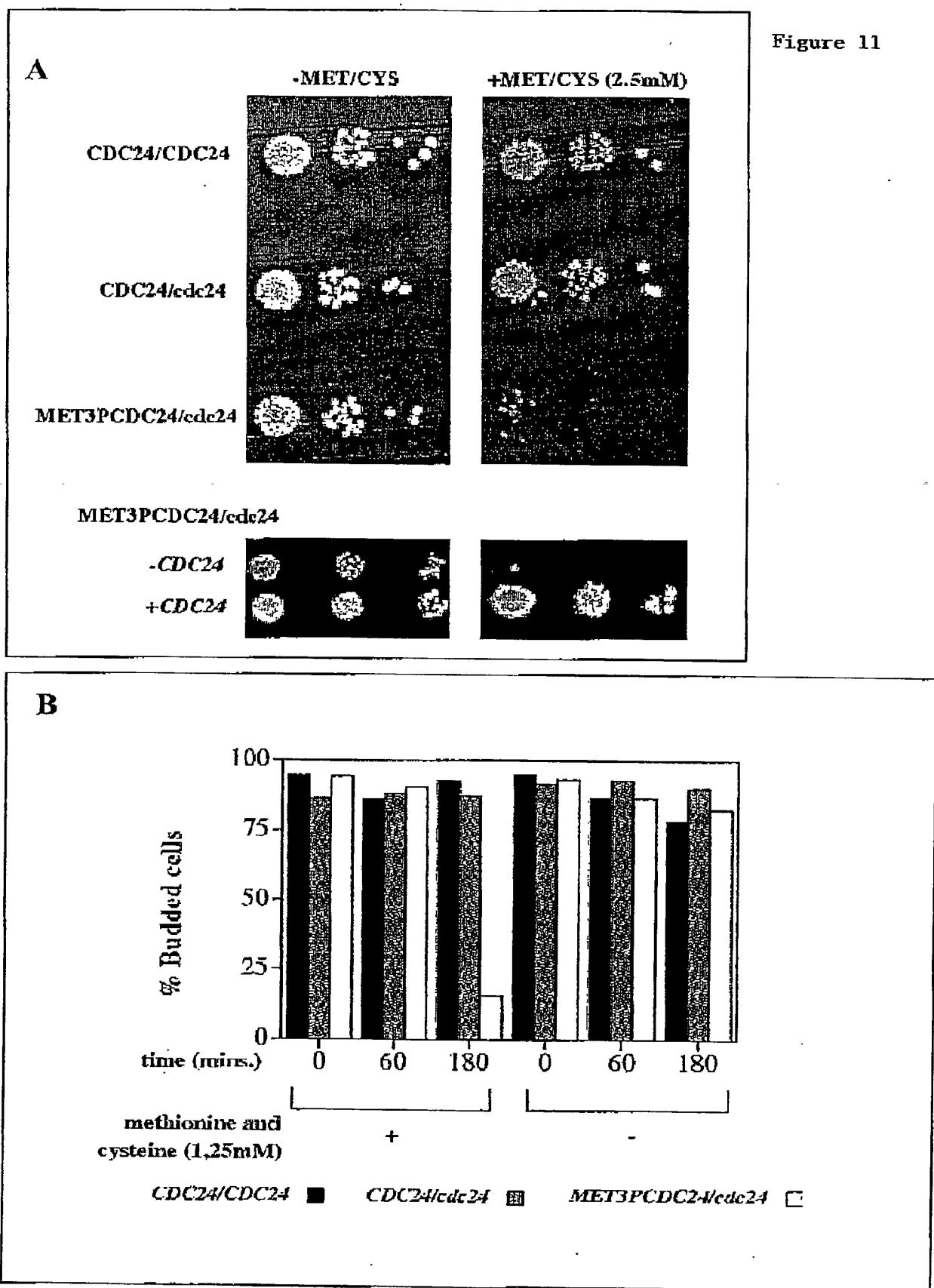
**Figure 10**

Figure 11



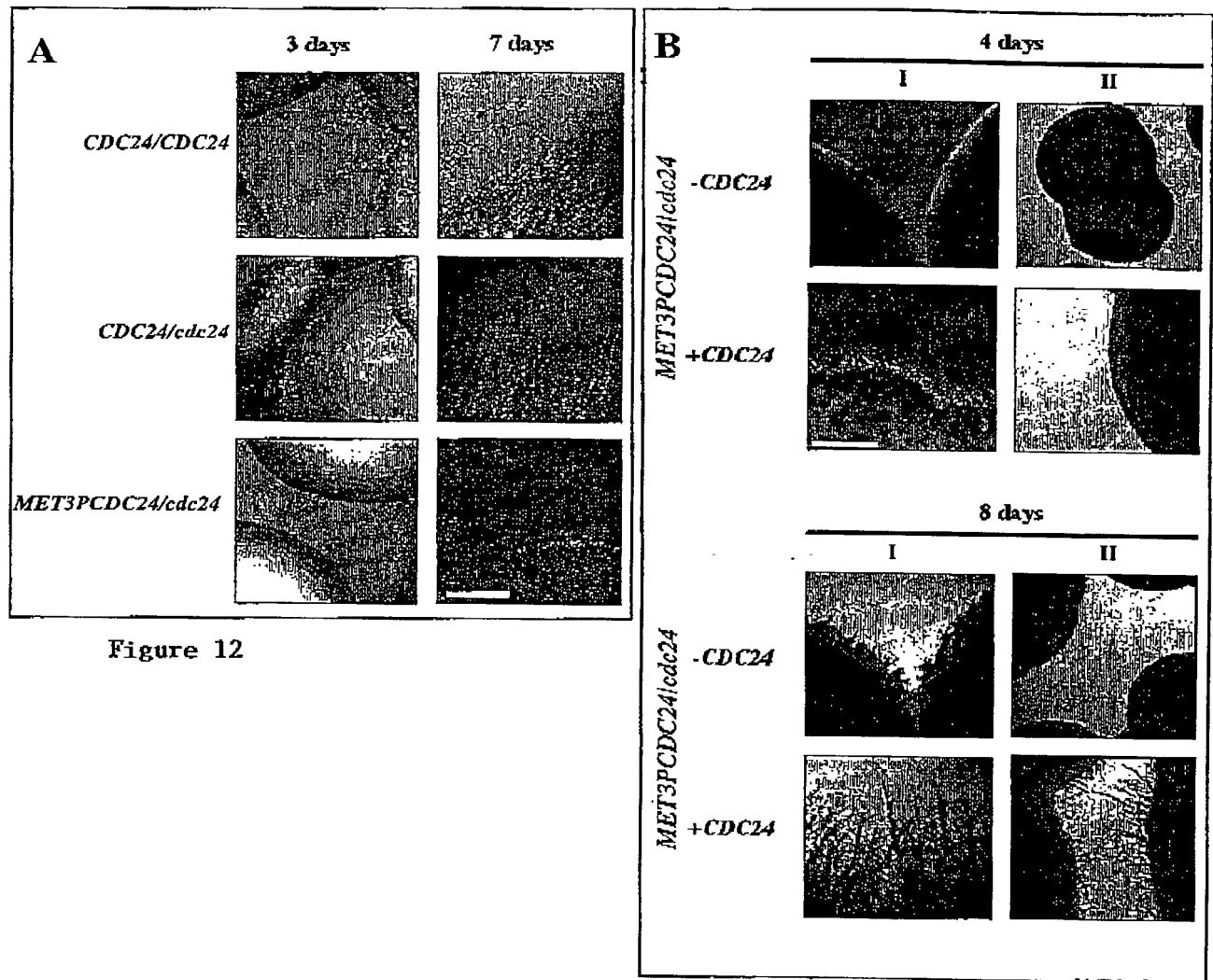
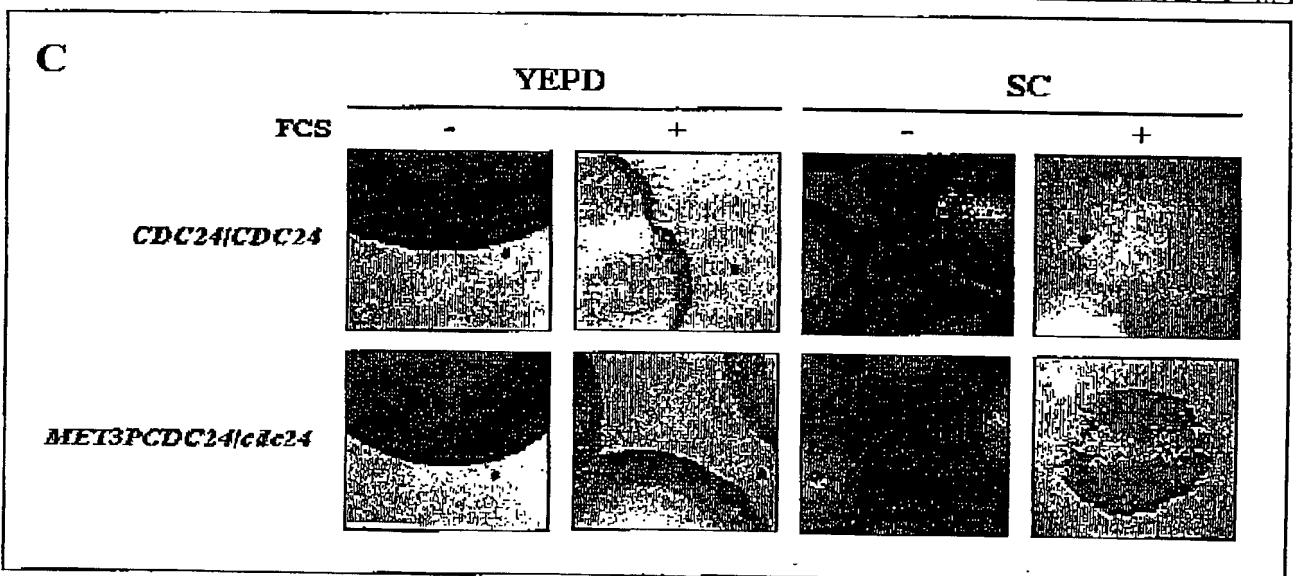


Figure 12



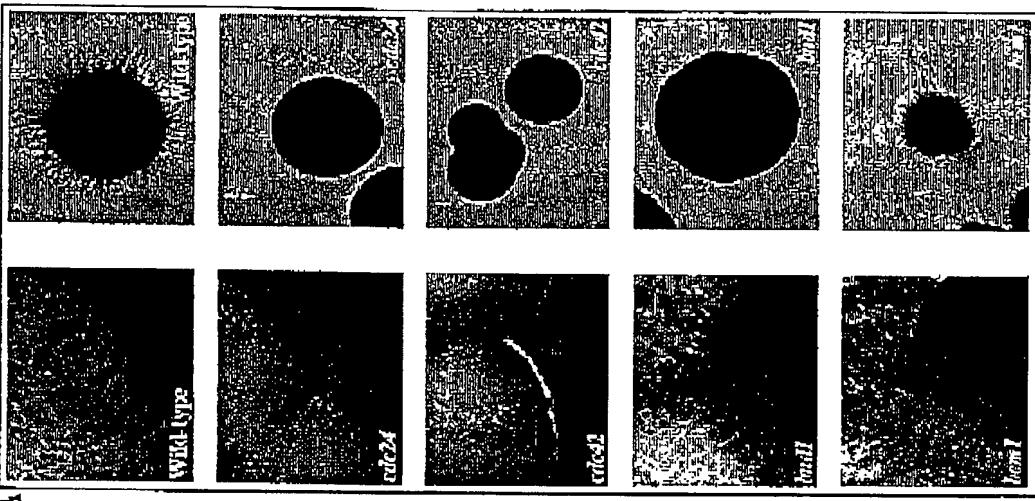


Figure 13

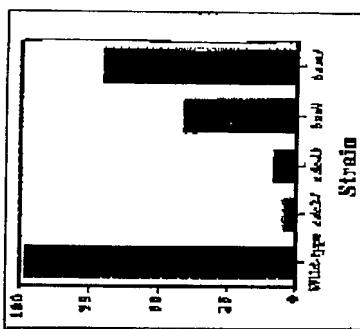
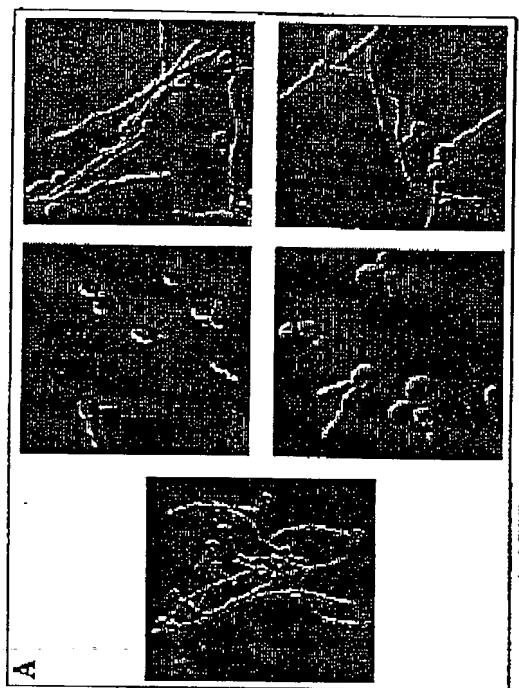


Figure 14B

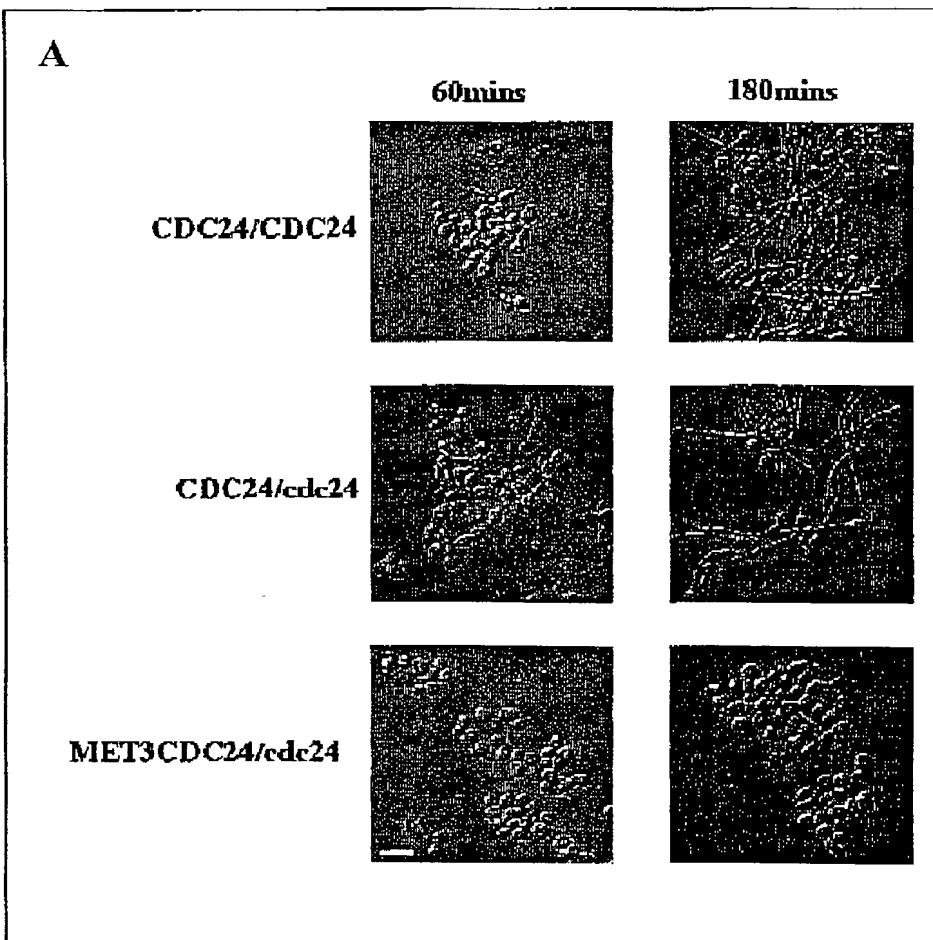
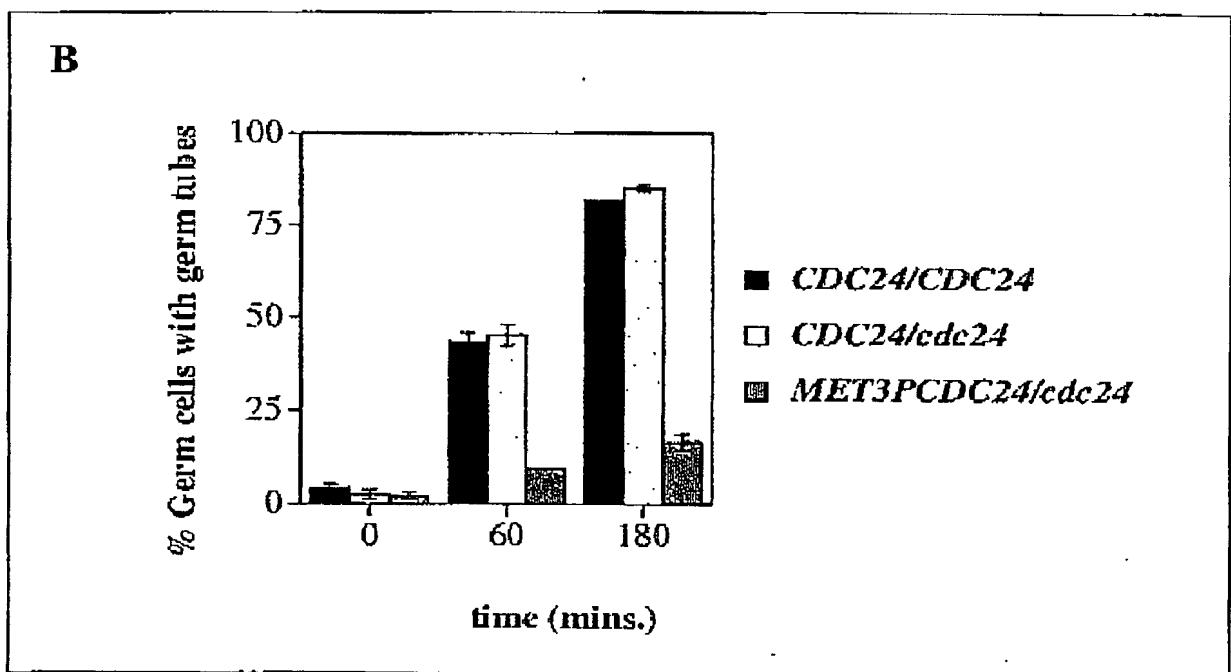
**Figure 15**

Figure 16

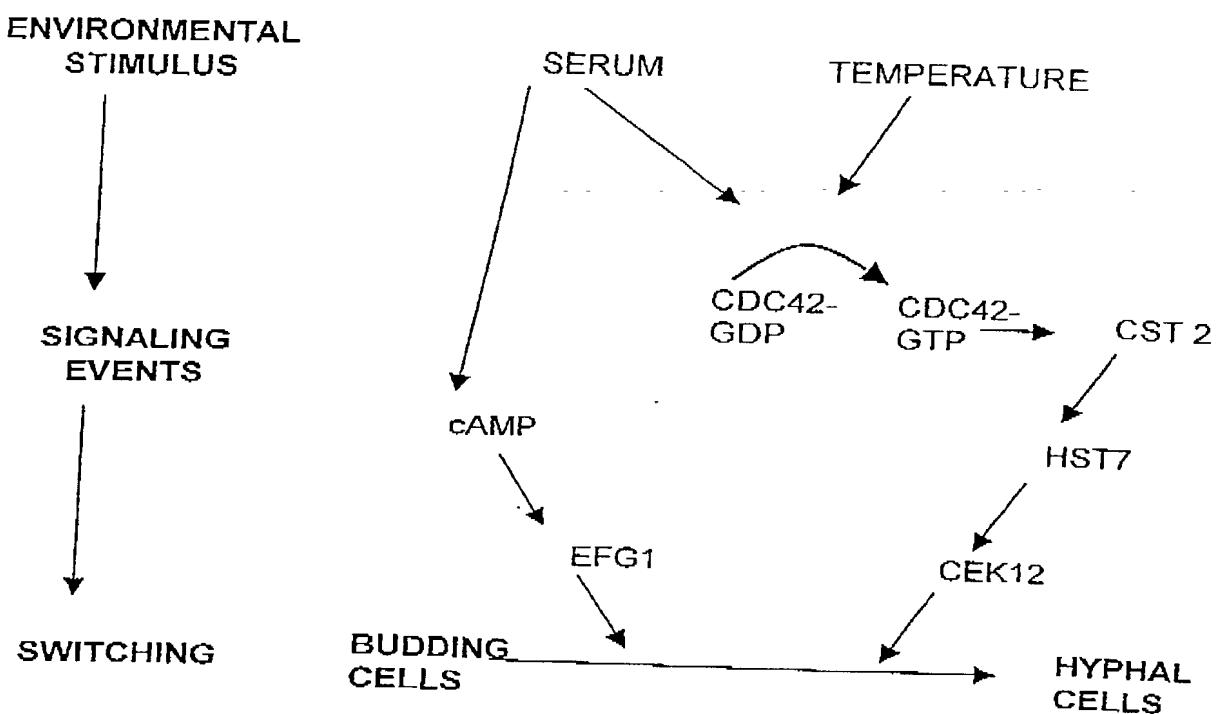


Figure 17

A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcatctgacgatttgaagtcgtaaaaaaaaatccatttatgactt  
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaaactcgacgtcccagctggtcaaagt  
gctagaagtagtagaaacgctaataitccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEVETLMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcatttgcacgatttgaagtcgtaaaaaaaaatccatttatgactt  
atattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaaactcgacgtcccagctggtcaaagt  
gctagaagtagtagaaacgctaataitccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEVETLMNSS

30

21/24

C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

ccccctctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcatctggcgatttgc  
tatattgggctgcaagaaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctggtcaaagt  
gctagaagttagtagaaacgctaataatccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHAFNDEELFTISDVFANSTSQ  
LVKVLEVVEETLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 cccctctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcacctgacgatttgc  
tatattgggctgcaagaaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctggtcaaagt  
gctagaagttagtagaaacgctaataatccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVIAPDDLKVCKKSIYDFILGCKKHAFNDEELFTISDVFANSTSQ  
LVKVLEVVEETLMNSS

22/24

## SEQ ID NO. 10

## STE4 DNA sequence (wild-type)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATAATACAAACCCAGTCTACAGGA  
 TAGCTCTGCAGTGGAGGAAGAAATTCAAAATAATAGAGGCCGCCAGACAAAGAGGTAAACRGCTTCATGCTCAARTA  
 ATTAAGCAAAACACAAAGATAACAAGATGCAAGCTTATTCCAGATGCCAACAAAGTCTCTCGTTGACCAAAATAAGATC  
 5 AACTTAAAGCCAAATATCGTGTCAAAGGCCATAATAATAAAATCTCAGATTTCGGTGGAGTCAGATTCAAAACGTAT  
 TTTGAGTGCAGTCAGATGGCTTATGCTTATATGGACAGTGCTTCAGGTTAAACAGAACGCTATTGCTTAGATT  
 CTCAATGGTTCTTCCTGCGCTATTCGCATCGAGTACTTGGTAGCAACCGCAGGATTAAACATAACTGTACCAT  
 TATAGAGTTTCAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTCAAAGGACATACTTGCTATATTCTGACAT  
 TGAAATTACAGATAACGCAATATATTGACAGCAAGTGGGGATATGACATGTGCCCTGGGGATACCGAAACCAAAGA  
 10 GGTTGAGAGAACTTCTGACCAATTAGGTGATGTTTGGCATTAGCTATTCTGAAAGAGCCAACCTAGAAATTCTTC  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTCATATGGGATAGCAGATCTCCGTCCTGTACAAAGCTTTA  
 CCTTAAACGAACTGCTATTATGGCACTTCGTTTTCTGAAAGGGGATGCTGAACTTGGAGGTTTGTAGAACGTTGG  
 TAAATATGTATGTTAAAGGTGGACTGTTCTACTGGTACTTTGCTTCTGAGGTTTGTAGAACGTTGGCTTGG  
 15 AACAAACCAAGGCGTTCTTAGATTTCGATCTGGAGTACAATAACCCGGCAATGGCACAAACTTTAAATGAAAGCTCAAGCTATCT  
 TTGGTGGGGATGTTAAAGGAGAGATTGTTGCAAATAAGTGGTCACTGGTGGCAAGTCACTGGTGTGCCCTCGAGT  
 CGAGATGGGTEAGCTGATGACAGGTTCAACGACTCAACCAATGAAATATGGTCTCCAGGTTTCAATAG  
 20

## SEQ ID NO. 11

## Ste4 Protein sequence (wild-type)

MHQMDSITYNNVTCOYIQPQSLQDISAVEEEIQNKIEARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTQNKEI  
 LKPNIVLKGEMNKISDERWSRDSKRILSASQDGPMLIWDSASCLQNAIPLDSQHVLSCAIESPSTLVASAGLNNNCTI  
 25 EYSKENRVAQWASIFKHTCYISDIEFTDNAHILTASGDMTCALWDIPKPKRVREYSDFHLGCVIALATFPEPNLENSI  
 CEASCGSDGYTIWDRSPSAVQSFYVNDDINALREFKDGMSTVAGSDNGAINMYDLRSDCSIATFSLFRGYEEARPT  
 TIVAAANMEYNTAQSPQTLXSTSSSYLDNQGVVSIDFSASGRILMYSCTDTIGCVVWDVILKGEEV3KLEGHGGRTGVRES  
 DGLAVCTGSWDSSTMKIWSPGYQ

30

## SEQ ID NO. 12

## ste4-o15 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATAATACAAACCCAGTCTACAGGA  
 35 TAGCTCTGCAGTGGAGGAAGAAATTCAAAATAATAGAGGCCGCCAGACAAAGAGGTAAACRGCTTCATGCTCAARTA  
 ATTAAGCAAAACACAAAGATAACAAGATGCAAGCTTATTCAGATGGCCAACAAAGTTACTTGCTTCAACAAATTAAGAT  
 AACTTAAAGCCAAATATCGTGTCAAAGGCCATAATAATAAAATCTCAGATTTCGGTGGAGTCAGATTCAAAACGTAT

TTTGAGTCAAGTCAAGATGGCTTATGCTTATATGGACAGTGCTCAGGTTAAACAGAACGCTATTCCATTAGA  
 5 CTCATGGGTTCTTCCTGCCTATTCGCCATCGAGTACCTTGGTAGCAGCGCAGGATTAACGCTATAACTGTACCAT  
 TATAGAGTTCGAAAGAAAACAGACTAGCGAAAACGTTGCGTCATTTCAAAGGACATACTTGGTATATTCTGACA  
 TGAATTTACAGATAACGCACATATATTGACAGCACTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG  
 10 GGGTGGAGAGGATATTCTGACCATTAGGTGATGTTGGCATTAGCTATTCTGAAGAGCCAACTTAGAAAATTCTTC  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTT  
 CGTTAACCGATAGTGTATTAATGCACTTCGTTTCAAAGACGGGATGTCGATTGTCAGGAAAGTGAACAATGGTGC  
 TAAATATGTATGATTTAAGGTGGACTGTTCTATTGCTACTTTCTCTTTCGAGGTTATGAAGAACGTACCCCTAC  
 CCTACTTATATGGCAGCTAACATGGACTACAATACCGCGCAATGCCACAACTTTAAATCAGCTGCTCAAGCTATC  
 15 AGACAACCAAGGCCTGTTCTTAGATTTAGTCATCTGGAAAGATTGATGTAACATGCTATAACAGACATGGTTGT  
 TTGTGTGGATGTTAAAGGAGAGATTGTTGAAAGGTCACTGGTGGCAGAGTCACTGGTGTGCGCTCGAG  
 CGAGATGGGTTAGCTGTATGTCAGGTTCATGGACTCACCATGAAATATGGCTCCAGGTTTCGAG  
 SEQ ID No. 13

## 15 Ste4-o15 Protein sequence (mutant)

MAHQMDSDITYSNNVTOQYIQPQLQDISAVEEEIQNKIEARQESKOLHAIINKAKHKIQLDASLPOMANKVTSLS  
 LKPNIVLKGNNKISDFRWSRDSKRILSASQDGFMILWDSASGLKQNAIPLDQSQWVLSCAISPSSTLVASAGLN  
 RVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTDASGDMTCALWDIPKAKRVRGYSDELGDVLA  
 20 TFASCGSDGYTYIWDSRSPSAVQSFYVNDSINALRFFKDGMSTIVAGSDNGAINMYDLRSDCSIATFSLFRGVEERTP  
 TYMAANMEVNTAQSPQTILKSTSSSYLDNQGVVSLDFASGRMLMYSCYTDCIGCVVWDVLKGIVVKLEGHGG  
 DGLAVCTGSDSTMKIWSPGYQ

## SEQ ID NO. 14

## 25 ste4-o17 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACACACAAAGTCTACAGGA  
 TATCTCTGAGTGGAGGAAGAAATTCAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTCATGCTCAATA  
 ATAAAGCTAAACACAAGATAACAAGATGCAAGCTTATCCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGAT  
 30 AACTTAAAGCCAAATATCGTGTGAAAGGCCATAATAATAAAATCTCAGATTTCGGTGGAGTCGAGATTCAAAACGTA  
 TTTGAGTCAAGTCAAGATGGCTTATGCTTATATGGGACAGTGCTCAGGTTAAACAGAACGCTATTCCATTAGAT  
 CTCAATGGTTCTTCCTGCGTATTCGCCATCGAGTACTTGGTAGCAGCGCAGGATTAAACATAACTGTACCAT  
 TATAGAGTTGCAAAACAGAGTACCGCAAAACGTTGCGTCACCTTGGAGACATACTTGGTATATTCTGACA  
 TGAAATTCAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG  
 35 GGGTGAGAGAAATTCTGACCATTAGGTGATGTTGGCATTAGCTATTCTGAAGAGCCAAACTTAGAAAATTCTTC  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCGTCCGCTGTACAAAGCTTT  
 CGTTAACCGATAGTGTATTAATGCACTTCGTTTCAAAGACGGGATGTCGATTGTCAGGAAAGTGAACATGCTGCG

TAAATATGATTAAGTCGGACTGTTCTATTGCTACTTTCTCTTTCGAGGTATGAAGAACGTACCCCTAC  
 CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATGCCACAAACTTAAAATCAACAAAGCTCAAGCTATCI  
 AGACAAACCAAGGGCGTGTCTTAGATTTAGTGCATCTGAAAGATTGATGACTCATGCTATAACAGACATTGGTTGTC  
 TTGTGTGGGATGTATTAAGGAGAGATTGGAAATTAGAAGGTATGGTGGCAGAGTCACTGGTGTGGCTCGAGI  
 5 CCAGATGGGTTAGCTGTATGTACAGGTTATGGGACTCAACCATGAAATATGGTCTCCAGGTTATCAATAG

## SEQ ID No. 15

Ste4-o17 Protein sequence (mutant)

10 MAHQMDSTIYSNNVTQQYIQPQLQDISAVEEEIQNKIEARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKII  
 LKPNIVLKGHNNKISDFRWSRDSKRILSASQDGFMILWDSASGLKQNAIPLDQSQWVLSCAISPSSTLVASAGLNNNCTI  
 RVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTAGDMTCALWDIPKPKRVREYSDHGDVIALRIPEEPNLNSSI  
 TFASCSDGYTYIWDSRSRSPSAVQSFYVNDSDINALRFFKDGMISIVAGSDNGAINMYDLRSDCSIAFSLFRGYEERTPTI  
 TYMAANMEYNTAQSPQTLKSTSSSYLDNQAVSLDFSASGRIMYSCTDYGCVWDVLKGEIVGKLEGHGRVTGVRSE  
 15 DGLAVCTGSWDSTMKIWSPGYQ

SEQ. I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ. I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly"

SEQ. I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ. I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ. I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ. I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ. I.D. No:22 refers to peptide sequence "QYEFDVILSPELKVQMKTI".